

Multiple QTL mapping in autopolyploids: a random-effect model approach with application in a hexaploid sweetpotato full-sib population

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Supplemental Tables

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Table S1 Proportion of mapped QTL paired to simulated positions (<20 cM, in percentage) and precision (absolute difference between simulated and mapped QTL peak position, on average, in centiMorgans) from 1,000 simulated quantitative traits with three QTLs with different heritabilities ($h_q^2 = \{0.27, 0.18, 0.09\}$) for three difference scenarios. Fixed-effect interval mapping (FEIM) and random-effect multiple interval mapping (REMIM) were carried out with and without the simulated error, under different genome-wide significance α level thresholds in 'Beauregard' \times 'Tanzania' (BT) full-sib population genetic map

Scenario	α	h_q^2	With error				Without error			
			FEIM		REMIM		FEIM		REMIM	
			Paired	Precision	Paired	Precision	Paired	Precision	Paired	Precision
Unlinked	0.20	0.3	95.20	2.32	97.20	2.62	99.90	0.55	100.00	0.77
		0.2	86.10	3.36	90.80	3.24	99.30	1.30	100.00	0.77
		0.1	48.70	4.76	67.60	4.57	88.30	3.04	100.00	0.56
	0.15	0.3	94.80	2.30	97.20	2.55	99.90	0.55	99.90	0.62
		0.2	84.50	3.34	89.80	3.03	99.20	1.30	99.90	0.52
		0.1	46.40	4.68	65.80	4.50	87.10	3.00	99.90	0.49
	0.10	0.3	94.40	2.31	97.00	2.54	99.90	0.55	99.90	0.60
		0.2	82.50	3.31	89.10	3.01	99.00	1.30	99.90	0.53
		0.1	41.70	4.57	64.10	4.45	86.30	2.99	99.90	0.49
	0.05	0.3	93.50	2.27	96.50	2.53	99.90	0.55	99.90	0.60
		0.2	80.00	3.25	88.10	3.01	98.80	1.28	99.90	0.52
		0.1	38.80	4.44	60.20	4.34	85.20	2.97	100.00	0.48
	0.01	0.3	91.60	2.21	94.50	2.43	99.80	0.55	99.90	0.59
		0.2	75.10	3.18	83.40	2.93	98.20	1.26	99.90	0.51
		0.1	28.40	4.30	49.00	4.13	81.40	2.86	99.90	0.48
Random	0.20	0.3	93.80	2.24	94.80	2.60	98.70	0.49	100.00	0.76
		0.2	83.10	3.36	89.70	3.28	94.40	1.33	100.00	0.83
		0.1	43.90	4.73	60.00	4.32	79.80	2.83	100.00	0.51
	0.15	0.3	93.50	2.21	94.80	2.39	98.80	0.49	99.90	0.47
		0.2	81.80	3.34	89.30	3.20	94.40	1.33	100.00	0.60
		0.1	41.90	4.79	58.60	4.32	79.30	2.81	100.00	0.47
	0.10	0.3	93.00	2.19	94.40	2.34	98.80	0.49	99.90	0.46
		0.2	79.80	3.31	88.30	3.18	94.20	1.31	100.00	0.58
		0.1	38.70	4.69	57.10	4.22	78.50	2.76	100.00	0.48
	0.05	0.3	92.20	2.18	93.80	2.32	98.80	0.49	99.90	0.46
		0.2	78.40	3.23	87.30	3.15	94.20	1.31	100.00	0.57
		0.1	36.20	4.66	54.20	4.15	77.20	2.75	99.90	0.47
	0.01	0.3	89.20	2.15	91.40	2.26	98.70	0.49	99.90	0.45
		0.2	72.80	3.13	83.90	3.06	94.10	1.32	100.00	0.55
		0.1	27.10	4.57	43.50	4.16	72.40	2.56	99.90	0.47
Linked	0.20	0.3	87.80	2.45	94.50	2.86	90.10	0.60	100.00	0.82
		0.2	67.90	3.09	89.10	3.19	70.60	1.06	100.00	0.86
		0.1	36.30	4.66	61.60	4.35	45.50	2.87	100.00	0.60
	0.15	0.3	87.60	2.43	94.70	2.49	90.10	0.60	100.00	0.51
		0.2	67.20	3.08	89.00	3.07	70.70	1.06	99.70	0.57
		0.1	34.70	4.63	60.50	4.10	45.60	2.88	100.00	0.54
	0.10	0.3	87.70	2.44	94.40	2.52	90.10	0.60	100.00	0.50
		0.2	67.70	3.07	88.30	2.99	70.80	1.06	99.60	0.55
		0.1	33.40	4.44	58.80	4.09	45.50	2.85	100.00	0.55
	0.05	0.3	86.80	2.40	93.90	2.49	90.20	0.60	100.00	0.50
		0.2	66.50	3.09	86.80	3.00	71.30	1.07	99.70	0.54
		0.1	28.90	4.32	55.30	4.06	45.80	2.72	100.00	0.55
	0.01	0.3	85.60	2.37	92.30	2.46	90.10	0.58	100.00	0.49
		0.2	62.50	2.96	82.00	2.91	71.60	1.07	99.70	0.53
		0.1	24.90	4.43	45.30	3.97	44.20	2.71	100.00	0.54

Table S2 Detection power, empirical false discovery rate (FDR) and coverage (all in percentage) relative to support intervals calculated for each $d = \{1.0, 1.5, 2.0\}$ from 1,000 simulated quantitative traits for three different scenarios. Fixed-effect interval mapping (FEIM) and random-effect multiple interval mapping (REMIM) were carried out with and without the simulated error, under different genome-wide significance α level thresholds in 'Beauregard' \times 'Tanzania' (BT) full-sib population genetic map

Scenario	α	d	With error						Without error						
			FEIM			REMIM			FEIM			REMIM			
			Power	FDR	Coverage	Power	FDR	Coverage	Power	FDR	Coverage	Power	FDR	Coverage	
Unlinked	0.20	1.0	65.3	23.5	85.2	79.7	15.2	93.5	88.5	14.0	92.3	99.7	8.1	99.7	
		1.5	72.1	15.4	94.0	82.7	12.1	97.0	93.2	9.5	97.3	99.8	8.1	99.8	
		2.0	75.0	12.0	97.8	83.9	10.8	98.5	94.9	7.9	99.1	99.8	8.1	99.8	
	0.15	1.0	64.1	21.6	85.2	78.0	14.7	92.6	88.1	12.5	92.4	99.9	5.3	100.0	
		1.5	70.8	13.3	94.2	80.9	11.5	96.0	92.8	7.9	97.3	99.9	5.3	100.0	
		2.0	73.7	9.8	98.0	82.1	10.4	97.4	94.5	6.3	99.1	99.9	5.3	100.0	
	0.10	1.0	62.2	20.0	85.4	77.1	13.5	92.5	87.8	11.1	92.4	99.9	4.8	100.0	
		1.5	68.7	11.6	94.3	80.0	10.3	95.9	92.5	6.6	97.3	99.9	4.8	100.0	
		2.0	71.4	8.2	98.0	81.1	9.1	97.3	94.2	4.9	99.1	99.9	4.8	100.0	
	0.05	1.0	60.4	18.8	85.3	75.5	12.3	92.5	87.4	10.1	92.4	99.9	4.2	100.0	
		1.5	66.7	10.3	94.3	78.5	9.0	96.2	92.0	5.5	97.3	99.9	4.2	100.0	
		2.0	69.3	6.9	98.0	79.4	7.9	97.3	93.7	3.8	99.1	99.9	4.2	100.0	
	0.01	1.0	55.5	16.7	85.4	70.2	9.6	92.8	86.1	8.7	92.4	99.9	3.5	100.0	
		1.5	61.3	8.2	94.2	72.8	6.4	96.3	90.6	4.1	97.3	99.9	3.5	100.0	
		2.0	63.7	4.6	98.0	73.5	5.4	97.2	92.3	2.4	99.1	99.9	3.5	100.0	
	Random	0.20	1.0	64.2	23.6	87.3	76.4	14.7	93.7	84.2	16.1	92.6	99.5	7.4	99.5
			1.5	69.8	17.0	94.8	79.2	11.7	97.2	88.1	12.4	96.9	99.7	7.3	99.7
			2.0	72.2	14.1	98.1	80.3	10.5	98.5	89.8	10.7	98.7	99.7	7.3	99.7
		0.15	1.0	63.1	21.8	87.2	74.7	14.7	92.3	84.0	14.6	92.5	100.0	4.0	100.0
			1.5	68.6	15.1	94.7	77.8	11.4	96.2	88.0	10.8	96.8	100.0	4.0	100.0
			2.0	71.0	12.1	98.1	78.7	10.4	97.3	89.7	9.1	98.7	100.0	4.0	100.0
		0.10	1.0	61.7	19.8	87.5	73.9	13.9	92.4	83.8	12.7	92.6	100.0	3.5	100.0
			1.5	66.9	13.3	94.9	76.8	10.6	96.1	87.7	8.8	96.9	100.0	3.5	100.0
			2.0	69.2	10.3	98.1	77.7	9.6	97.3	89.4	7.0	98.8	100.0	3.5	100.0
0.05		1.0	60.2	18.3	87.4	72.4	12.5	92.3	83.4	11.4	92.6	99.9	3.2	100.0	
		1.5	65.4	11.6	94.8	75.4	9.1	96.1	87.3	7.4	96.9	99.9	3.2	100.0	
		2.0	67.7	8.6	98.2	76.3	8.0	97.3	88.9	5.7	98.7	99.9	3.2	100.0	
0.01		1.0	55.3	15.7	87.7	67.7	10.3	92.8	82.1	9.3	92.9	99.9	2.8	100.0	
		1.5	59.9	9.2	95.0	70.3	6.9	96.3	85.7	5.6	96.9	99.9	2.8	100.0	
		2.0	61.9	6.3	98.1	71.1	5.9	97.4	87.3	3.9	98.8	99.9	2.8	100.0	
Linked		0.20	1.0	55.4	23.2	86.5	76.2	15.0	93.2	64.0	16.0	93.2	99.8	7.9	99.8
			1.5	60.1	16.7	93.9	79.1	11.9	96.7	66.9	12.4	97.3	99.9	7.9	99.9
			2.0	62.4	13.6	97.5	79.8	11.1	97.7	67.9	11.0	98.8	99.9	7.9	99.9
		0.15	1.0	54.6	21.5	86.5	75.4	14.1	92.6	64.0	14.5	93.0	99.9	4.9	100.0
			1.5	59.3	14.7	93.9	78.5	10.7	96.4	66.9	10.6	97.2	99.9	4.9	100.0
			2.0	61.5	11.6	97.4	79.2	9.9	97.3	68.0	9.1	98.8	99.9	4.9	100.0
		0.10	1.0	54.5	20.4	86.6	74.1	13.5	92.1	64.0	12.9	93.0	99.9	4.4	100.0
			1.5	59.2	13.5	94.0	77.2	10.0	95.9	66.9	8.9	97.2	99.9	4.4	100.0
			2.0	61.3	10.4	97.4	78.0	9.1	96.9	68.0	7.4	98.8	99.9	4.4	100.0
	0.05	1.0	52.9	17.9	87.2	72.5	12.1	92.1	64.3	10.1	93.1	99.9	3.9	100.0	
		1.5	57.3	10.9	94.4	75.3	8.8	95.8	67.2	6.1	97.3	99.9	3.9	100.0	
		2.0	59.2	8.1	97.5	76.2	7.8	96.8	68.3	4.6	98.9	99.9	3.9	100.0	
	0.01	1.0	50.4	16.6	87.3	67.4	10.7	92.1	63.8	8.3	93.0	99.9	3.4	100.0	
		1.5	54.4	9.7	94.3	70.0	7.4	95.6	66.7	4.4	97.2	99.9	3.4	100.0	
		2.0	56.1	6.8	97.3	70.7	6.5	96.6	67.8	2.9	98.8	99.9	3.4	100.0	

Table S3 Summary of fixed-effect interval mapping (FEIM) for eight yield-related traits in ‘Beauregard’ × ‘Tanzania’ (BT) full-sib family. Linkage group (LG), map position (in centiMorgans) and its ~95% support interval (within parenthesis), likelihood-ratio test (LRT), its corresponding logarithm of the odds (LOD) and the adjusted R^2 (R^2_{adj} , in percentage) are shown for each mapped QTL using permutation-based genome-wide significance LOD threshold of 0.05.

Trait ^a	QTL	LG	Position (cM)	LRT	LOD	R^2_{adj} (%)
NOCR	1	1	144.57 (100.30-154.00)	42.67	9.27	10.32
	2	3	20.18 (16.60-45.54)	45.04	9.78	11.03
NONC	1	3	32.56 (4.68-50.15)	38.27	8.31	8.99
	2	10	111.40 (97.02-151.19)	38.87	8.44	9.17
	3	15	56.86 (40.40-78.04)	47.78	10.37	11.85
	4	15	119.08 (88.03-120.03)	39.03	8.48	9.22
TNR	1	1	143.01 (130.55-156.18)	46.72	10.15	11.53
	2	3	32.56 (18.43-44.03)	49.77	10.81	12.43
	3	15	77.15 (41.12-127.15)	40.06	8.70	9.53
CYTHA	1	15	5.34 (0.00-38.38)	42.56	9.24	10.29
RYTHA	1	15	5.34 (0.00-38.38)	40.56	8.81	9.68
FYTHA	1	10	25.11 (16.12-133.55)	36.42	7.91	8.42

^a Trait abbreviations: number of commercial (NOCR), noncommercial (NONC) and total (TNR) roots per plant, commercial (CYTHA), noncommercial (NCYTHA) and total (RYTHA) root yield in $t \cdot ha^{-1}$, foliage yield (FYTHA) in $t \cdot ha^{-1}$, and commercial index (CI).

Table S4 Additive allele effects from QTL mapped for eight yield-related traits in ‘Beauregard’ × ‘Tanzania’ (BT) full-sib family using random-effect multiple interval mapping (REMIM). ‘Beauregard’ ($\{a, \dots, f\}$) and ‘Tanzania’ ($\{g, \dots, l\}$) alleles represent the parental contribution to the trait mean.

Trait ^a	QTL	‘Beauregard’						‘Tanzania’					
		<i>a</i>	<i>b</i>	<i>c</i>	<i>d</i>	<i>e</i>	<i>f</i>	<i>g</i>	<i>h</i>	<i>i</i>	<i>j</i>	<i>k</i>	<i>l</i>
NOCR	1	-0.0565	0.0901	-0.0388	-0.0040	0.0299	-0.0206	-0.0142	0.0232	-0.0010	0.0603	-0.0931	0.0248
	2	0.0048	-0.0094	-0.0975	0.0910	-0.0273	0.0385	-0.1370	0.0194	0.0032	0.0807	0.0112	0.0225
NONC	1	-0.0543	0.0290	0.0211	-0.0032	0.0321	-0.0247	-0.0133	0.0335	-0.0171	0.0783	-0.0753	-0.0061
	2	0.0450	-0.0180	-0.0629	0.0391	-0.0258	0.0226	-0.0281	0.0040	-0.0281	0.0229	-0.0347	0.0639
	3	-0.0146	0.0029	-0.0379	-0.0564	0.0135	0.0926	-0.0539	-0.0130	0.0385	0.0480	0.0605	-0.0800
	4	-0.0662	0.0031	0.0362	-0.0281	-0.0185	0.0734	-0.0206	0.1195	-0.0135	-0.0065	-0.0172	-0.0618
TNR	1	-0.1080	0.1184	0.0059	-0.0141	0.0619	-0.0642	-0.0378	0.0566	-0.0330	0.1181	-0.1579	0.0540
	2	0.0870	-0.0300	-0.2240	0.1565	-0.0573	0.0678	-0.2291	0.0203	-0.0305	0.1474	-0.0124	0.1042
	3	0.0840	-0.0036	0.0037	-0.1326	0.0034	0.0451	-0.0996	0.0697	0.0308	0.0242	0.0875	-0.1126
	4	-0.0888	0.1187	0.0071	-0.0364	-0.0838	0.0832	-0.1121	0.2083	0.0327	-0.0207	-0.0621	-0.0461
CYTHA	1	0.3436	0.7652	-0.6404	-0.1211	-0.1671	-0.1803	0.0551	0.2210	1.0067	-0.3285	-0.4530	-0.5013
RYTHA	1	0.3217	0.8136	-0.6961	-0.1137	-0.2138	-0.1117	0.0492	0.3144	0.9903	-0.3734	-0.3922	-0.5882
FYTHA	1	-0.2765	-0.1241	0.2158	0.0181	-0.0849	0.2517	-0.1770	-0.6752	0.2976	0.1144	0.2364	0.2039

^a Trait abbreviations: number of commercial (NOCR), noncommercial (NONC) and total (TNR) roots per plant, commercial (CYTHA), noncommercial (NCYTHA) and total (RYTHA) root yield in $t \cdot ha^{-1}$, foliage yield (FYTHA) in $t \cdot ha^{-1}$, and commercial index (CI).

Table S5 Map (in centiMorgans) and genome (in base pairs) positions and support intervals (inside the parentheses) for QTL mapped in 'Beauregard' × 'Tanzania' full-sib family using random-effect multiple interval mapping (REMIM) for eight yield-related traits.

Trait ^a	QTL	LG	Map position (cM)	<i>I. trifida</i> genome (bp)	<i>I. triloba</i> genome (bp)
NOCR	1	1	137.60 (99.43-152.87)	21766797 (15917835-23289854)	26312289 (10387174-28126436)
	2	3	20.18 (0.00-49.27)	1591872 (32030-3664896)	1802096 (22131-4090763)
NONC	1	1	142.07 (128.08-159.30)	22334649 (20332569-24033209)	26960935 (6568909-29323516)
	2	3	13.11 (0.00-51.33)	806480 (32030-3972955)	917422 (22131-4646213)
	3	10	102.26 (96.50-113.55)	18827245 (18241193-19647452)	22932891 (22254345-23849899)
	4	15	67.20 (39.10-78.04)	4437217 (2225465-5613152)	4956558 (2534197-6405520)
TNR	1	1	140.43 (128.08-152.87)	22187065 (20332569-23289854)	26810127 (6568909-28126436)
	2	3	20.18 (13.11-43.69)	1591872 (806480-3417617)	1802096 (917422-3825133)
	3	10	165.43 (102.26-187.27)	23304855 (18827245-24516154)	27542198 (22932891-28845769)
	4	15	78.04 (35.50-119.08)	5613152 (1976149-17701006)	6405520 (2282565-21381416)
CYTHA	1	15	5.34 (0.00-34.27)	477772 (21822-1915814)	570552 (56000-2213276)
RYTHA	1	15	5.34 (0.00-35.50)	477772 (21822-1976149)	570552 (56000-2282565)
FYTHA	1	10	29.09 (16.12-134.37)	2508929 (1518491-21555353)	2930617 (1398004-25560274)

^a Trait abbreviations: number of commercial (NOCR), noncommercial (NONC) and total (TNR) roots per plant, commercial (CYTHA), noncommercial (NCYTHA) and total (RYTHA) root yield in t · ha⁻¹, foliage yield (FYTHA) in t · ha⁻¹, and commercial index (CI).